DOCKET NO.: 078728/0106



Figure 1: Restriction pattern of the HAL coding region cut with selected enzymes.

### HAL

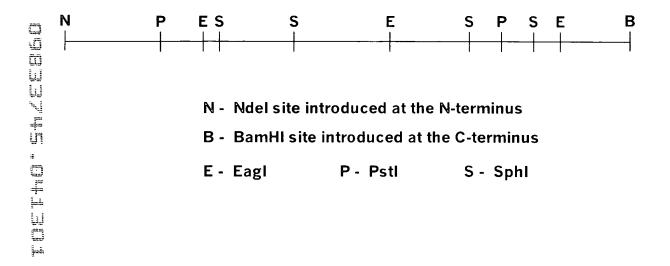


Figure 2: Experimentally derived peptide sequences of HAL

N-terminal

(M)ASAPQITLGLSGATAD

Internal

(M)ALADLDELLDEA

(M)GEPVEREVLRA

Figure 3: SphI digestion pattern of HAL gene showing oligonucleotide and subclones.

### HAL

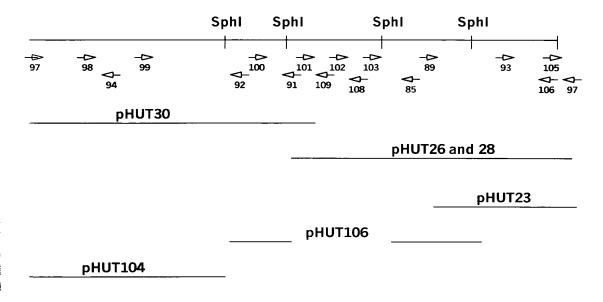


Figure 4: Histidine ammonia lyase overexpressing plasmid.

### pHUT102

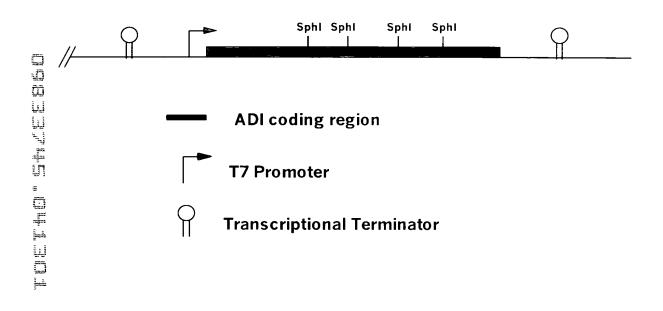
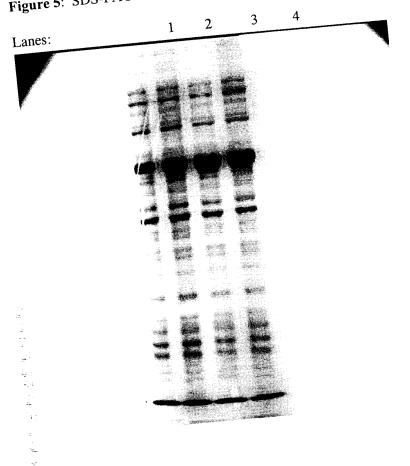


Figure 5: SDS-PAGE showing expression of HAL in E. coli.



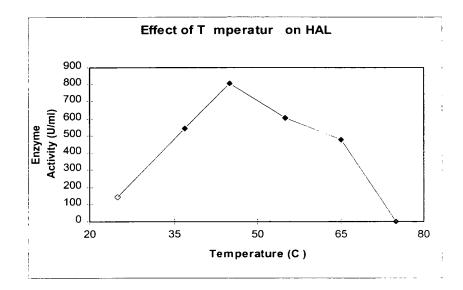
Title: CLONING, OVEREXPRESSION AND THERAPEUTIC USE OF BIOACTIVE HISTIDINE AMMONIA LYASE

Inventor(s): Joseph ROBERTS et al DOCKET NO.: 078728/0106

Figure 6: SDS-PAGE showing purification of HAL from E. coli



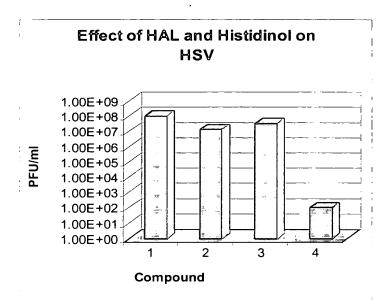
Figure 7: Effect of Temperature on HAL



THERAPEUTIC USE OF BIOACTIVE
HISTIDINE AMMONIA LYASE
Inventor(s): Joseph ROBERTS et al.
DOCKET NO.: 078728/0106

Figure 8: Effect of pH on HAL.

Figure 9: Effect of HAL and Histidinol on HSV.



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Figure 10: Effectiveness of L-histidinol as a Single Agent

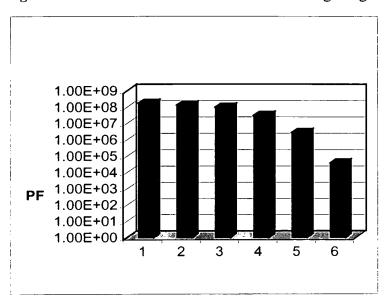


Figure 11: Effect of HAL and Histidinol on RSV.

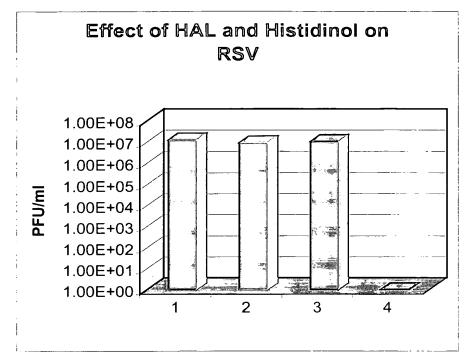
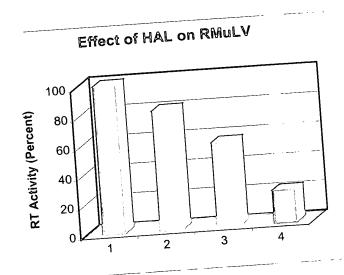


Figure 12: Effect of HAL on RMuLV.



E Tomas

### Figure 13: Histidine ammonia lyase peptide sequence pileup

	unan bashi			
	HUTH_PSEPU			
	HUTH_RHIME			
	HUTH_MOUSE MPRYTVHVRGEWLAVE HUTH RAT	PCQDGKLTVGWLGREA	/RRYMKNKPDNGGFTSVD	EVQFLVHRCKG
	_	CQDGKLSVGWLGREA	JRRYMKNKPDNGGFTSVD	EVRFLVRRCKG
	MPRYTVHVRGEWLAVI HUTH_CAEEL LPLADDYFEVRRTVG HUTH_BACS		/RRYIKNKPDNGGFTSVD PCKP-DDTIHAVAKKSVE	
	_			
	HUTH_STRGR			
	HUTH_CORY			
	HUTH_PSEPU			
O	- HUTH_RHIME			
u	- HUTH_MOUSE	LGLLDNEDELEVALE	ONEFVEVVIEGDVMS	PDFIPSQPEGVFLYSKYR
J	HUTH_RAT	LGLLDNEDLLEVALE	ONEFVEVVIEGDVMS	PDFIPSQPEGVFLYSKYR
	HUTH_HUMAN	LGLLDNEDRLEVALE	NNEFVEVVIEGDAMS	PDFIPSQPEGVYLYSKYR
	HUTH_CAEEL NSLLDPEDLVSDVLKI HUTH_BACS	)SDFIIVAASVEETEDA	AKEAKKQEEIDNARAEIE	KIDNRRRKVSF
U	HUTH_STRGR			
į.	HUTH_CORY			
	-			
	IIIMI DOEDII			
	HUTH_PSEPU TELTLKPGTLTLAQLI	RAIHAAPVRLQLDASAA	APAIDASVACVEQIIA	
	HUTH_RHIME	 ETIYWTGAPARLDAAFI	DAGTAKAAARTAETVA	
	HUTH_MOUSE			
	EPEKYIALDGDSLSTI HUTH RAT	DLVNLGKGRYKIKLT:	SIAEKKVQQSREVIDSII	K
	EPEKYIALDGDSLST	EDLVNLGKGHYKIKLT:	SIAEKKVQQSREVIDSII	K
	HUTH_HUMAN EPEKYIELDGDRLTTI		PTAEKRVQKSREVIDSII	K
	HUTH_CAEEL	TI DONGLI DEDIVAC	ENCECTIOI CMECEDDID	KADELI EKTAC
	HUTH_BACS		EKGECAIQLSMESEDRIR	RANIF LENIAS
	MVTLDGSSLTTADVAI HUTH STRGR	RVLFDFEEAAASEESMI	ERVKKSRAAVERIVR	
	MDMHTVVVGTSGTTA		<b>AAA</b> VEALAAARLIVDALA	A
	HUTH_CORY MASAPQITLGLSGATA	ADDVIAVARHEARISI	SPQVLEELASVRAHIDAL	AS

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### Figure 13 cont'd.

EDRTAYGINTGFGLLASTRIASHDLENLQRSLVLSHAAGIGAPLDDDLVRLIMVLKINSL

GNAPVYGINTGFGKLASIKIDSSDVATLQRNLILSHCCGVGQPLTEDIVRLIMALKLISL

ERTVVYGITTGFGKFARTVIPANKLQELQVNLVRSHSSGVGKPLSPERCRMLLALRINVL

ERTVVYGITTGFGKFARTVIPANKLQELQVNLVRSHSSGVGKPLSPERCRMLLALRINVL

EKTVVYGITTGFGKFARTVIPINKLQELQVNLVRSHSSGVGKPLSPERCRMLLALRINVL

EHRAVYGVTTGFGTFSNVTIPPEKLKKLQLNLIRSHATGYGEPLAPNRARMLLALRINIL

DEKTIYGINTGFGKFSDVLIQKEDSAALQLNLILSHACGVGDPFPECVSRAMLLLRANAL

KPEPVYGVSTGFGALASRHIGTELRAQLQRNIVRSHAAGMGPRVEREVVRALMFLRLKTV

ADTPVYGISTGFGALATRHIAPEDRAKLQRSLIRSHAAGMGEPVEREVVRALMFLRAKTL

SRGFSGIRRKVIDALIALVNAEVYPHIPLKGSVGASGDLAPLATMSLVLLGEGKARYKGQ

GRGASGVRLELVRLIEAMLDKGVIPLIPEKGSVGASGDLAPLAHMAAVMMGHGEAFFAGE HUTH\_MOUSE

AKGYSGISLETLKQVIEAFNASCLSYVPEKGTVGASGDLAPLSHLALGLIGEGKMWSPKS

AKGYSGISLETLKQVIEVFNASCLSYVPEKGTVGASGDLAPLSHLALGLIGEGKMWSPKS

AKGYSGISLETLKQVIEMFNASCLPYVPEKGTVGASGDLAPLSHLALGLVGEGKMWSPKS

AKGHSGISVENIKKMIAAFNAFCVSYVPQQGTVGCSGDLCPLAHLALGLLGEGKMWSPTT

HUTH\_BACS LKGFSGVRAELIEQLLAFLNKRVHPVIPQQGSLGASGDLAPLSHLALALIGQGEVFFEGE

ASGHTGVRPEVAQTMADVLNAGITPVVHEYGSLGCSGDLAPLSHCALTLMGEGEAEGPDG HUTH\_STRGR

VRPVVLETMVGMLNAGITPVVREYGSLGCSGDLAPLSHCALVLMGEGEATDAHG

WLSATEALAVAGLEPLTLAAKEGLALLNGTQASTAYALRGLFYAEDLYAAAIACGGLSV

 ${\tt RMKGDAALKAAGLSPVTLAAKEGLALINGTQVSTALALAGLFRAHRAGQAALITGALST}$ 

GWADAKYVLEAHGLKPIVLKPKEGLALINGTQMITSLGCEALERASAIARQADIVAALTL

GWADAKYVLEAHGLKPIVLKPKEGLALINGTQMITSLGCEAVERASAIARQADIVAALTL

GWADAKYVLEAHGLKPVILKPKEGLALINGTQMITSLGCEAVERASAIARQADIVAALTL

 ${\tt GWQPADVVLKKNNLEPLELGPKEGLALINGTQMVTALGAYTLERAHNIARQADVIAALSL}$ 

RMPAMTGLKKAGIQPVTLTSKEGLALINGTQAMTAMGVVAYIEAEKLAYQTERIASLTI

TVRPAGELLAAHGIAPVELREKEGLALLNGTDGMLGMLVMALADLRNLYTSADITAALSL

DIRPVPELFAEAGLTPVELAEKEGLALVNGTDGMLGQLIMALADLDELLDIADATAAMSV

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Figure 13 cont'd.

HUTH PSEPU

EAVLGSRSPFDARIHE-ARGORGOIDTAACFRDLLGDSSEVSLSHKNCD----

KVODPYS

HUTH RHIME

DAAMGSSAPFHPDIOH-CAAIRARSTRAAALROLLTG-SPIROSHIEGDE-~-

RVODPYC

HUTH MOUSE

EVLKGTTKAFDTDIHA-VRPHRGQIEVAFRFRSLLDS-

DHHPSEIAESHRFCDRVQDAYT

HUTH RAT

EVLKGTTKAFDTDIHA-VRPHRGOIEVAFRFRSLLDS-

DHHPSEIAESHRFCDRVODAYT

HUTH HUMAN

EVLKGTTKAFDTDIHA-LRPHRGOIEVAFRFRSLLDS-

DHHPSEIAESHRFCDRVQDAYT

HUTH CAEEL

DVLKGTTRAYDPDIHR-IRPHRGQNLSALRLRALLHS-

EANPSQIAESHRNCTKVQDAYT

HUTH BACS

EGLQGIIDAFDEDIHL-ARGYQEQIDVAERIRFYLSD-SGLTTSQGE----

LRVQDAYS

HUTH STRGR

EALLGTDKVLAPELHA-IRPHPGQGVSADNMSRVLAG-SGLTGHHODDAP---

RVQDAYS

HUTH CORY

EAQLGTDQVFRAELHEPLRPHPGQGRSAQNMFAFLAD-SPIVASHREGDG---

RVQDAYS

HUTH PSEPU

LRCQPQVMGACLTQLRQAAEVLGIEANAVSDNPLVFAAEGDVISGGNFHAEPVAMAADNL

HUTH\_RHIME

IRCQPQVDGACLDLLRSVAATLTIEANAVTDNPLVLSDN-

SVVSGGNFHAEPVAFAADQI

HUTH\_MOUSE

LRCCPQVHGVVNDTIAFVKDIITTELNSATDNPMVFASRGETISGGNFHGEYPAKALDYL

U HUTH RAT

LRCCPQVHGVVNDTIAFVKDIITTELNSATDNPMVFASRGETISGGNFHGEYPAKALDYL

HUTH HUMAN

I LRCCPQVHGVVNDTIAFVKNIITTELNSATDNPMVFANRGETVSGGNFHGEYPAKALDYL

HUTH CAEEL

LRCVPQVHGVVHDTIEFVREIITTEMNSATDNPLVFADREEIISGGNFHGEYPAKALDFL

HUTH\_BACS

LRCIPOVHGATWOTLGYVKEKLEIEMNAATDNPLIFNDGDKVISGGNFHGOPIAFAMDFL

HUTH STRGR VRCAPQVNGAGRDTLDHAALVAGRELASSVDNPVVLPDG-

RVESNGNFHGAPVAYVLDFL

HUTH CORY LRCSPQVTGAARDTIAHARLVATRELAAAIDNPVVLPSG-

EVTSNGNFHGAPVAYVLDFL

HUTH PSEPU ALAIAEIGSLSERRISLMMDKHMS-

QLPPFLVENGGVNSGFMIAQVTAAALASENKALSH

HUTH RHIME

ALAVCEIGAISQRRIALLVDPALSLRLPAFLAKKPGLNSGLMIAEVTSAALMSENKQLSH

HUTH MOUSE AIGVHELAAISERRIERLCNPSLS-

ELPAFLVAEGGLNSGFMIAHCTAAALVSESKALCH

HUTH RAT ELPAFLVAEGGLNSGFMIAHCTAAALVSESKALCH

AIGVHELAAISERRIERLCNPSLS-

HUTH HUMAN AIGIHELAAISERRIERLCNPSLS-

ELPAFLVAEGGLNSGFMIAHCTAAALVSENKALCH

HUTH CAEEL AIAVAELAQMSERRLERLVNKELS-GLPTFLTPDGGLNSGFMTVQLCAASLVSENKVLCH

HUTH BACS

KIAISELANIAERRIERLVNPQLN-

DLPPFLSPHPGLQSGAMIMQYAAASLVSENKTLAH

HUTH STRGR

AIVAADLGSICERRTDRLLDKNRSHGLPPFLADDAGVDSGLMIAQYTQAALVSEMKRLAV

HUTH CORY

AIAVADLGSIAERRTDRMLDPARSRDLPAFLADDPGVDSGMMIAQYTQAGLVAENKRLAV

### Figure 13 cont'd.

	HUTH_PSEPU HUTH_RHIME HUTH_MOUSE HUTH_RAT HUTH_HUMAN HUTH_CAEEL HUTH_BACS HUTH_STRGR	PHSVDSLPTSANQEDHVSMAPAAGKRLWEMAENTRGVPAIEWLGACQGLDLRKG—LKTS PASVDSTPTSANQEDHVSMACHGARRLLQMTENLFSIIGIEALAAVQGIEFRAP—LTTS PSSVDSLSTSAATEDHVSMGGWAARKALRVVEHVEQVLAIELLAACQGIEFLRP—LKTT PSSVDSLSTSAATEDHVSMGGWAARKALRVIEHVEQVLAIELLAACQGIEFLRP—LKTT PSSVDSLSTSAATEDHVSMGGWAARKALRVIEHVEQVLAIELLAACQGIEFLRP—LKTT PSSVDSIPTSCNQEDHVSMGGFAARKALTVVEHVEAVLAMELLAACQGIEFLKP—LIST PASVDSIPSSANQEDHVSMGTIAARHAYQVIANTRRVIAIEAICALQAVEYRGI—EHAA
		HVSMGWSAARKLRTAVDNLARIVAVELYAATRAIELRAAEGLTPA
	HUTH_CORY	PA-VDSIPSSAMQEDHVSLGWHAARKLPTSVANLRRILAVEMLIAGRALDLRAP-LKPG
	HUTH_PSEPU	AKLEKARQALRSEVA-HYDRDRFFAPDIEKAVELLAKGS-LTGLLPAGVLPSL
	HUTH RHIME	PELQKAAAAVRGVSS-SIEEDRYMADDLKAAGDLVASGR-LAAAVSAGILPKLEN-
	HUTH_MOUSE	TPLEKVYDLVRSVVR-
	PWIKDRFMAPDIEAA	HRLLLDQKVWEVAAPYIEKYRMEHIPESR
	HUTH_RAT	TPLEKVYDLVRSVVR-
		HRLLLDQKVWEVAAPYIEKYRMEHIPESR
	HUTH_HUMAN	TPLEKVYDLVRSVVR-
		HRLLLEQKVWEVAAPYIEKYRMEHIPESR
	HUTH_CAEEL	APLHKIYQLVRSVAP-
		LEMIRENRIWEAVLPHLETLEAMEELDPD
q	HUTH_BACS	SYTKQLFQEMRKVVP-SIQQDRVFSYDIERLTDWLKKESLIPDHQNKELRGMNI-
1	HUTH_STRGR	PASEAVVAALRAAGAEGPGPDRFLAPDLAAADTFVREGR-LVAAVEPVTGPLA
	HUTH_CORY	PATGAVLEVLRSKVA-GPGQDRFLSAELEAAYDLLANGS-VHKALEAHLPE
U	HUTH PSEPU	
= : =	HUTH RHIME	
	HUTH MOUSE	PLSPTAFSLESLRKNSATIPESDDL
300 100	HUTH RAT	PLSPTAFSLESLRKNSATIPESDDL
	HUTH HUMAN	PLSPTAFSLQFLHKKSTKIPESEDL
	HUTH CAEEL	ALRQFTKTPTGIVQDRSMIPISDDEESIE
빞	HUTH BACS	
	HUTH STRGR	
ļab	HUTH_CORY	

80

-----VPLHHLADIYWNNGSAKLDPSFDAAVLKGAARIAEIAAGNAPVYGINTGFGKLASIKIDAADLATLQ ----MVTLDGSSLTTADVARVLFDFEEAAASEESMERVKKSRAAVERIVRDEKTIYGINTGFGKFSDVLIQKEDSAALQ ---TELTLKPGTLTLAQLRAIHAAPVRLQLDASAAPAIDASVACVEQIIAEDRTAYGINTGFGLLASTRIASHDLENLQ MASAPOITLGLSGATADDVIAVARHEARISISPQVLEELASVRAHIDALASADTPVYGISTGFGALATRHIAPEDRAKLO ---MHTVVVGTSGVTASDVLAVARAGARIELSEEAVAALAAARSVVDALAAARPDVYGVSTGFGALATRHISPELRGRLQ -MDMHTVVVGTSGTTAEDVVAVARHGARVELSAAAVEALAAARLIVDALAAARPEPVYGVSTGFGALASRHIGTELRAQLQ -----MILDRDLNLEQFISVVRHGEQVELSAAARERIARARTVIEQIVEGDTPIYGVNTGFGKFENVQIDRSQLAQLQ -----VPLHHLADIYWNNGSAKLDPSFDAAVLKGAARIAEIAAGNAPVYGINTGFGKLASIKIDAADLATLQ ---MLHLMIKPGQLSLKQLRQVSRSPVVLSLDPEAIPAIAESAQVVEQVISEGRTVYGINTGFGLLANTKIAPQDLETLQ ----MSLHLKPGQLTLADLRQAYLAPVRLSLDPSADAPIAASVACVENIIAEGRTAYGINTGFGLLASTRISPADLEKLQ --MTNLKELDGRSLSLHDLHRIIYEGETVGASDESMEKVKQSRKAVEQIVADEKIIYGITTGFGKFSDIFIDPDDVENLQ ----LRPGSVPLSDLETIYWTGAPARLDAAFDAGIAKAAARIAEIVAGNAPVYGINTGFGKLASIKIDSSDVATLQ MSDLPSVVFGDGFLRWQELVAVARHGARLELSAAAWARIDNARAIVCRIVANGERAYGISTGLGALCDVLLEGEOLAELS KYREPEKY IELDGLTTEDLVNLGKGRYKIKLTPTAEKRVQKSREV IDSI I KEKTVVYGITTG FGK FA-RTVI PINKLOLO VLAPPTKLLILDGNSPEDLVRCEKGECAIQLSMESEDRIRKARTFLEKIASEHRAVYGVTTGFGTFSNVT1PPEKLKKLQ ----MIEIDGRSLRVEDVYAVAVEYDRVSISDDTLKAVEEKHEAFLKLINSGKTVYGVNTGFGSLLNVHIERDQEIELQ KYREPEKYIALDGDSTEDLVNLGKGRYKIKLTSIAEKKVQQSREVIDSIIKERTVVYGITTGFGKFA-RTVIPANKLQLQ KYREPEKYIALDGDSTEDLVNLGKGRYKIKLTSIAEKKVQQSREVIDSIIKERTVVYGITTGFGKFA-RTVIPANKLQLQ KYREPEKY IALDGDSTEDLVNLGKGHYKIKLTS IAEKKVQQSREV IDSI IKERTVVYGITTGFGKFA-RTVI PANKLQLQ ---MNALTLIPGTLTLAQLRQVWQQPLQLTLDESAHEAINDSVACVEAIVAEGRTAYGINTGFGLLAQTRIATHDLENLQ ---MGEMISLDGPLTWREIASIAEGASLDLSGPARLRIAQARRIVDALVERGIRGYGINTGVGALCDVIISRENQQALS ---MSDTRIDAADREALQ

> 41.78 40.68 40.78

> > SWALL: HUTH RHIME

11

 $SWALL: Q9HU\overline{9}0$ 

SWALL: HUTH PSEPU

10 12

SWALL: Q9KBE6

38.8%

SWALL:HUTH\_HUMAN SWALL:HUTH\_CAEEL SWALL:Q9HLI6

SWALL: HUTH MOUSE

SWALL: BAB29407 SWALL: HUTH RAT SWALL: AAG53586

113 114 116 119 119

SWALL: Q9KKE0

SWALL: 09HQD5

41.0% 38.68 38.68 38.2% 39.8% 38.9%

39.2%

# 

## Figure 14

65.48 46.8% 42.0%

SWALL: HUTH STRGR SWALL: HUTH DEIRA

SWALL: CAC21618

SWALL:BAB16159

SWALL: Q9KWE4

100.0% 66.18 42.0% 40.48 42.28 41.78 39.3%

SWALL: HUTH BACSU

SWALL: Q9KSQ4

SWALL: Q9HU85

ω

## Figure 14, cont'd

160 RNLILSHCCGVGQPLTEDIVRLIMALKLISLGRGASGVRLELVRLIEAMLDKGVIPLIPEKGSVGASGDLAPLAHMAAVM RSLIRSHAAGMGEPVEREVVRALMFLRAKTLASGRTGVRPVVLETMVGMLNAGITPVVREYGSLGCSGDLAPLSHCALVL RNIVRSHAAGMGPRVEREVVRALMFLRLKTVCSGRTGVRPEVAQTMADVLNAGITPVVHEYGSLGCSGDLAPLSHCALTL RNIVRSHAAGMGPRVEREVVRALMFLRLKTVASGHTGVRPEVAQTMADVLNAGITPVVHEYGSLGCSGDLAPLSHCALTL HNLIVSHAIGMGEPLPAEVVRGMLLLRAQSLSLGHSGVRVEVVELLLALLNADALPVVPSQGSVGASGDLAPLAHLALGL RNLILSHCCGVGAPLPENVVRLIMALKLISLGRGASGVRIELIRLIEGMLEKGVIPVIPEKGSVGASGDLAPLAHMSATM RNLILSHCCGVGAPLPENVVRLIMALKLISLGRGASGVRIELIRLIEGMLEKGVIPVIPEKGSVGASGDLAPLAHMSATM LNLILSHACGVGDPFPECVSRAMLLLRANALLKGFSGVRAELIEQLLAFLNKRVHPVIPQGGSLGASGDLAPLSHLALAL KSIVLSHAAGIGELMSDETVRLMMLLKINSLARGYSGIRLEVIQALIELVNNQIYPCVPKKGSVGASGDLAPLAHMSTVL RSIVLSHAAGVGEALDDAMVRLVMLLKVNSLARGFSGIRRKVIDALIALINAEVYPHIPLKGSVGASGDLAPLAHMSLVL HNLIYSHACGVGSPFPETVSRTMLVLRANALLKGFSGVRPLVIERLLALVNANIHPVIPQQGSLGASGDLAPLSHLALVL RSLVLSHAAGIGAPLDDDLVRLIMVLKINSLSRGFSGIRRKVIDALIALVNAEVYPHIPLKGSVGASGDLAPLAHMSLVL RNTLLSHACGVGEPLRDEOTRAIICAAVANYSOGKSGLDRSLVEGLLALLNHGITPOVPAOGSVGY---LTHMAHVGIAL VNLVRSHSSGVGKPLSPERCRMLLALRINVLAKGYSGISLETLKQVIEMFNASCLPYVPEKGTVGASGDLAPLSHLALGL LNLIRSHATGYGEPLAPNRARMLLALRINILAKGHSGISVENIKKMIAAFNAFCVSYVPQQGTVGCSGDLCPLAHLALGL KNLIRSHSSGVGDYLENRYVRAIMAVRLNSLAAGYSAVSADLLNNMVEMLNRDVIPAVPKYGSVGASGDLAPLAHIGLAM VNLVRSHSSGVGKPLSPERCRMLLALRINVLAKGYSGISLETLKQVIEAFNASCLSYVPEKGTVGASGDLAPLSHLALGL VNLVRSHSSGVGKPLSPERCRMLLALRINVLAKGYSGISLETLKQVIEAFNASCLSYVPEKGTVGASGDLAPLSHLALGL VNLVRSHSSGVGKPLSPERCRMLLALRINVLAKGYSGISLETLKQVIEVFNASCLSYVPEKGTVGASGDLAPLSHLALGL RSLVLSHAAGVGEPLDDDIVRLMMVLKINSLARGFSGIRLSVIQALIALVNAGVYSVDPAKGSVGASGDLAPLAHMSLTL RNIILSHACGVGDPLGRVEARAVMAAQIANLTHGYSGVRVETAEMLLALLNADIIPLIPSRGSVGY-----LTHAALVL ANLVRSHAAGAGSELDTAAVRALLVTRLNALAKGYSGIRERVLDVLVGLLNEGVHPVVPSRGSLGASGDLAPLAHMSRVL 81 65.48 46.88 42.0% 42.0% 40.48 42.28 41.78 39.3% 41.78 40.68 40.78 39.2% 38.8% 41.0% 38.68 38.68 38.2% 66.18 39.8% 38.9% 100.0% SWALL: HUTH\_STRGR SWALL: HUTH\_DEIRA SWALL: HUTH BACSU SWALL: HUTH PSEPU SWALL: HUTH RHIME SWALL: Q9HU90 SWALL: HUTH HUMAN SWALL: HUTH MOUSE SWALL: HUTH CAEEL SWALL: BAB16159 SWALL: CAC21618 SWALL: BAB29407 SWALL: HUTH RAT SWALL: AAG53586 SWALL: Q9KBE6 SWALL:09HLI6 SWALL: Q9KWE4 SWALL: Q9KSQ4 SWALL: Q9HU85 SWALL: Q9KKE0 SWALL: Q9HQD5 983831 10 12 20 20 20 20 20 20 20

# 

# Figure 14, cont'd.

	161		40
7	.00.08	MGEGEATDAHGDIRPVPELFAEAGLTPVELAEKEGLALVNGTDGMLGQLIMALADLDELLDIADATAAMSVEAQLGTDQV	
	66.1%	MGEGDAEGPDGTVRPAGELLAAHGIAPVELREKEGLALLNGTDGMLGMLVMALADLDTLYKSADITAALTMEALLGTDRV	
	65.48	MGEGEAEGPDGTVRPAGELLAAHGIAPVELREKEGLALLNGTDGMLGMLVMALADLRNLYTSADITAALSLEALLGTDKV	
	46.8%	IGLGDI-EYQGQVRPAADVLAELGLSPVQLQAKEGLALINGTQLMGSLLALALHDAQVLLGTANLAAAMTVEARYGSHRP	
	42.0%	MGEGEAF-YQGVQMPSKDALAKAGLSPVVLAAKEGLALINGTQTSTALALAGLFRAHRAAQSALVTGALSTDAAMGSSAP	
	42.0%	MGEGEAF-YQGVQMPSKDALAKAGLSPVVLAAKEGLALINGTQTSTALALAGLFRAHRAAQSALVTGALSTDAAMGSSAP	
	40.48	IGQGEVF-FEGERMPAMTGLKKAGIQPVTLTSKEGLALINGTQAMTAMGVVAYIEAEKLAYQTERIASLTIEGLQGIIDA	
	42.28	LGEGQAR-YNGKIISGLEAMKIAGLEPITLAPKEGLALLNGTQASTAFALEGLFVAEDLFASATVCGAMSVEAALGSRRP	
	41.78	IGESRARH-RGEWLPAAEALAVAGLEPLTLAAKEGLALLNGTQVSTAYALRGLFEAEDLFAAATVCGGLSVEAMLGSRAP	
	39.3%	LGEGEVF-YKGTKTKASFALKEEEIEPITLTAKEGLALINGTQAMTAMGVIAYLEAEKLAFQSEIIASLTMEGLRGIIDA	
	41.78	LGEGKAR-YKGQWLSATEALAVAGLEPLTLAAKEGLALLNGTQASTAYALRGLFYAEDLYAAAIACGGLSVEAVLGSRSP	
	40.68	MGHGEAFFAGERMKGDAALKA-AGLSPVTLAAKEGLALINGTQVSTALALAGLFRAHRAGQAALITGALSTDAAMGSSAP	
	40.78	LGIGEVS-YRGSVVPAAAALAAEGLATVRLGAKDGLCLVNGTPCMTGLACLALDDAQRLAQWADVIGAMSFEALRGQLAA	
	39.2%	VGEGKMWSPKSGWADAKYVLEAHGLKPVILKPKEGLALINGTQMITSLGCEAVERASAIARQADIVAALTLEVLKGTTKA	
	38.8%	LGEGKMWSPTTGWQPADVVLKKNNLEPLELGPKEGLALINGTQMVTALGAYTLERAHNIARQADVIAALSLDVLKGTTRA	
	41.0%	MGEGKAF-FEGRLMDSARALEKAGLKPYQFKEKEGVALINGTSFMSGILSIAVMDAHDILENAIRSALLSFEALGGTSKA	
	38.68	IGEGKMWSPKSGWADAKYVLEAHGLKPIVLKPKEGLALINGTQMITSLGCEALERASAIARQADIVAALTLEVLKGTTKA	
	38.68	IGEGKMWSPKSGWADAKYVLEAHGLKPIVLKPKEGLALINGTQMITSLGCEALERASAIARQADIVAALTLEVLKGTTKA	
	38.2%	IGEGKMWSPKSGWADAKYVLEAHGLKPIVLKPKEGLALINGTQMITSLGCEAVERASAIARQADIVAALTLEVLKGTTKA	
	39.8%	LGEGKAR-YRGEWLPAATALQKAGLAPVTLAAKEGLALLNGTQASTAFALRGLFEAEDLFASAVVCGALTTEAVLGSRRP	
	38.9%	IGHGSAMQGTERLSGADAL-ARLGLAPLRLEAKEGLSLVNGTPCATGLAALALARTERLFAWADAAAAMTYE-NLGSQAN	
	42.28	IGEGQA-DVAGERMPAAEALAAADLEPVTLQAKEGLALINGTQLTTGVAALALVDAERVLRSADTAGALTTEVTMSTTAS	

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### Title: CLONING, OVEREXPRESSION AND THERAPEUTIC USE OF BIOACTIVE HISTIDINE AMMONIA LYASE Inventor(s): Joseph ROBERTS et al. DOCKET NO.: 078728/0106

## Figure 14, cont'd.

	241	3	320
983831	100.08	FRAELHEPLRPHPGQGRSAQNMFAFLADSPIVASHREGDGRVQDAYSLRCSPQVTGAARDTIAHARLVATRELAAAIDNP	
1 SWALL: CAC21618	66.18	LAPELHA-IRPHPGQAASAANMAAVLKGSGLTGHHQDDAPRVQDAYSVRCAPQVAGAGRDTMAHAGLVAERĒLAAAVDNP	
2 SWALL: HUTH STRGR	65.48	LAPELHA-IRPHPGQGVSADNMSRVLAGSGLTGHHQDDAPRVQDAYSVRCAPQVNGAGRDTLDHAALVAGRELASSVDNP	
3 SWALL: HUTH DEIRA	46.8%	FQPDV-VGLRPHPGALAVAAELREFLAGSEIAPSHLTGDGKVQDAYSLRAVPQVHGATWDALAQAERVLAVEFASVTDNP	
4 SWALL:BAB16159	42.0%	FHPDIHT-LRGHKGQIDAGSALRNLLQGSEIRESHIEGDERVQDPYCIRCQPQVDGACLDLLASVARTLEIEANAVTDNP	
5 SWALL:Q9KWE4	42.0%	FHPDIHT-LRGHKGQIDAGSALRNLLQGSEIRESHIEGDERVQDPYCIRCQPQVDGACLDLLASVARTLEIEANAVTDNP	
6 SWALL: HUTH BACSU	40.48	FDEDIHLA-RGYQEQIDVAERIRFYLSDSGLTTSQGELRVQDAYSLRCIPQVHGATWQTLGYVKEKLEIEMNAATDNP	
7 SWALL:Q9KSQ4	42.28	FDPRIHR-VRGHRTQMDAATAYRHLLVSSEIGQSHSNCE-KVQDPYSLRCQPQVMGACLQQIRSAAEVLEVEANSVSDNP	
8 SWALL:Q9HU35	41.78	FDARIHAA-RGQRGQIDVAAAYRDLLASSEVARSHEKCD-KVQDPYSLRCQPQVMGACLTQMRQAAEVLEIEANAVSDNP	
9 SWALL:Q9KBE6	39.3%	FDEQIHFA-RGYVEQVDVARRMESYLQDSQLTTRQGELRVQDAYSLRCIPQVHGATWQTLRYVKEKLEIEMNAATDNP	
O SWALL: HUTH PSEPU	41.78	FDARIHEA-RGQRGQIDTAACFRDLLGDSSEVSSHKNCD-KVQDPYSLRCQPQVMGACLTQLRQAAEVLGIEANAVSDNP	
1 SWALL: HUTH RHIME	40.68	FHPDIQHCAAIRARSTRAAA-LRQLLTGSPIRQSHIEGDERVQDPYCIRCQPQVDGACLDLLRSVAATLTIEANAVTDNP	
2 SWALL:09HU90	40.78	FDAEI-VALKPHPGMQRVAANLRALLAGSQVLENARGIRTQDALSIRSIPQIHGACRDQLAHARQIET-ELNSATDNP	
3 SWALL: HUTH HUMAN	39.2%	FDTDIHA-LRPHRGQIEVAFRFRSLLSDSEIAESHRFCD-RVQDAYTLRCCPQVHGVVNDTIAFVKNIITTELNSATDNP	
4 SWALL: HUTH CAEEL	38.8%	YDPDIHR-IRPHRGQNLSALRLRALLNPSQIAESHRNCT-KVQDAYTLRCVPQVHGVVHDTIEFVREIITTEMNSATDNP	
5 SWALL:Q9HLI6	41.0%	FTPWILGA-RPHLGQVAIGNRFREYLTGSDIVKRADSVKVQDAYTLRCIPQVYGSVADVIDYVENVLSVEINSATDNP	
6 SWALL: HUTH MOUSE	38.6%	FDTDIHA-VRPHRGQIEVAFRFRSLLSDSEIAESHRFCD-RVQDAYTLRCCPQVHGVVNDTIAFVKDIITTELNSATDNP	
7 SWALL:BAB2 <u>9</u> 407	38.6%	FDTDIHA-VRPHRGQIEVAFRFRSLLSDSEIAESHRFCD-RVQDAYTLRCCPQVHGVVNDTIAFVKDIITTELNSATDNP	
8 SWALL:HUTH_RAT	38.2%	FDTDIHA-VRPHRGQIEVAFRFRSLLSDSEIAESHRFCD-RVQDAYTLRCCPQVHGVVNDTIAFVKDIITTELNSATDNP	
9 SWALL: AAG53586	39.8%	FDARIHE-VRGQRGQIDAAALFRHVLTDTSAIASHHNCD-KVQDPYSLRCQPQVMGACLTQMRQVAEVLLVESNAVSDNP	•
O SWALL:Q9KKEO	38.9%	AFAELPLALRQSPGLSAVGEGLRDWLADSPMLAGTAGTRTQDPLSLRAVPQVHGAARDAFGQVAEIVDRELASVTDNP	
1 SWALL:09HQD5	42.28	CAPAIHE-VRPHDGQAVSARHIRNLTAGSEVLDHHRDCD-RVQDAYSIRCLPQVHGAVRDALDHLRAAVATELNSATDNP	

# 

# Figure 14, cont'd.

	321		400
983831	100.0%	VVLPSGEVTSNGNFHGAPVAYVLDFLAIAVADLGSIAERRTDRMLDPARSRDLPAFLADDPGVDSGMMIAQYTQAGLVAE	
SWALL: CAC21618	66.1%	VVLPDGRVESNGNFHGAPVAYVLDFLAVAVADLGSIAERRTDRLLDKNRSHGLPPFLADDAGVDSGLMIAQYTQAALVGE	
SWALL: HUTH STRGR	65.48	VVLPDGRVESNGNFHGAPVAYVLDFLAIVAADLGSICERRTDRLLDKNRSHGLPPFLADDAGVDSGLMIAQYTQAALVSE	
SWALL: HUTH DEIRA	46.8%	LIFPTGEVVSGGNFHGQPLAVTIDALKVAVAELGSISERRTEQLLNPALS-GLPAFLTPNGGLNSGFMIAQYTSAALVSE	
SWALL:BAB16159	42.0%	LVLSDNSVVSGGNFHAEPVAFAADQTALAVCEIGAIAQRRIALLVDPALSYGLPAFLSKKPGLNSGLMIAEVTSAALMSE	
SWALL: Q9KWE4	42.0%	LVLSDNSVVSGGNFHAEPVAFAADQTALAVCEIGAIAQRRIALLVDPALSYGLPAFLSKKPGLNSGLMIAEVTSAALMSE	
SWALL: HUTH BACSU	40.48	LIENDGDVISGGNFHGQPIAFAMDFLKIAISELANIAERRIERLVNPQLN-DLPPFLSPHPGLQSGAMIMQYAAASLVSE	
SWALL: Q9KSQ4	42.28	LVFADGDIISGGNFHAEPVAMAADNLALAIAEIGSLSERRMALLIDSALSK-LPPFLVDNGGVNSGFMIAQVTAAALASE	
SWALL:Q9HU85	41.78	LVFAAGDVISGGNFHAEPVAMAADNLALALAEIGSLSERRISLMMDMHMSQ-LPPFLVANGGVNSGFMIAQVTAAALASD	
SWALL:Q9KBE6	39.3%	LIFDNGQVISGGNFHGQQIALAMDFLGIAMAELANISERRIERLVNPQLN-DLPPFLSAAPGVQSGVMILQYCAASLVSE	
SWALL: HUTH PSEPU	41.78	LVFAAGDVISGGNFHAEPVAMAADNLALAIAEIGSLSERRISLMMDKHMSQ-LPPFLVENGGVNSGFMIAQVTAAALASE	
SWALL: HUTH RHIME	40.68	LVLSDNSVVSGGNFHAEPVAFAADQIALAVCEIGAISQRRIALLVDPALSLRLPAFLAKKPGLNSGLMIAEVTSAALMSE	
SWALL: Q9HU90	40.78	LLLGTPEVVSQANPHGESVAMAADLLAIAVAELGGVAERRLDRLVNPLVS-GLPAFLVGKPGVNSGMMITQYVAASLAGE	
SWALL: HUTH HUMAN	39.2%	MVFANGETVSGGNFHGEYPAKALDYLAIGIHELAAISERRIERLCNPSLS-ELPAFLVAEGGLNSGFMIAHCTAAALVSE	
SWALL: HUTH CAEEL	38.8%	LVFADREIISGGNFHGEYPAKALDFLAIAVAELAQMSERRLERLVNKELS-GLPTFLTPDGGLNSGFMTVQLCAASLVSE	
SWALL:Q9HLI6	41.0%	L-FNGEEVVSGGNFHGEPVALAADFLAIALTDLGNMVERRIARLVDTNLS-GLPPFLTPDSGLNSGYMIPQYTAAALCNR	
SWALL: HUTH MOUSE	38.6%	MVFASGETISGGNFHGEYPAKALDYLAIGVHELAAISERRIERLCNPSLS-ELPAFLVAEGGLNSGFMIAHCTAAALVSE	
SWALL: BAB29407	38.6%	MVFASGETISGGNFHGEYPAKALDYLAIGVHELAAISERRIERLCNPSLS-ELPAFLVAEGGLNSGFMIAHCTAAALVSE	
SWALL: HUTH_RAT	38.2%	MVFASGETISGGNFHGEYPAKALDYLAIGVHELAAISERRIERLCNPSLS-ELPAFLVAEGGLNSGFMIAHCTAAALVSE	
SWALL: AAG53586	39.8%	LVFAANEMVFRGNFHAEPVAMAADNLALAIAEIGALSERRIALMMDKHMSQ-LPPFLVRNGGVNSGFMIAQVTAAALASE	
SWALL:Q9KKE0	38.98	AVAGSPEVHSQAHAVGAALGLAMDSLAVAVAEVAAISERRIDRLVNPLVS-GLPAFLAGDSGVSSGFMIAQYTAAALVAE	
SWALL:Q9HQD5	42.28	LVFPSGTVVSGGNFHGEVLALRLGYAASALAELAAISERRTDRLLNPETQEPLEPFLAPDSGLHSGLMIPQYTAASLVND	

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NRRLAAPASLDGGITSALÕEDMLTHATPAAWKALSIVDNLERILAIELLAAHRPMSCSRKRRARRNAPLPFTGTYARRSP lrslgqp-tldnasvsgaŏedhvsmsagaaynfreavekaatvvgvellcgaqgrefldplalgagtaaaydlvr-evse SKALCHPSSVDSLSTSAATEDHVSMGGWAARKALRVIEHVEQVLAIELLAACQGIEFLRPLKTTTPLEKVYDLVRSVVRP NKGLCHPTSVDK-PPSANQEDHVSMAPAAGRRLWEMAGNTRGVLAVEWLAACQGADLRDGLTSSPLLEQARQSCGEQVAH SKALCHPSSVDSLSTSAATEDHVSMGGWAARKALRVVEHVEQVLAIELLAACQGIEFLRPLKTTTPLEKVYDLVRSVVRP SKALCHPSSVDSLSTSAATEDHVSMGGWAARKALRVVEHVEQVLAIELLAACQGIEFLRPLKTTTPLEKVYDLVRSVVRP NKVLAYPSSADTIPTSANÕEDHVSMGATGSLKLLEIIDNVRYIIAIEYLLGSÕALEFTDK-GMSPSTRKIYĒKIREKVEK NKALCHPSSVDSLSTSAATEDHVSMGGWAARKALRVIEHVEQVLAIELLAACQGIEFLRPLKTTTPLEKVYDLVRSVVRP NKVLCHPSSVDSIPTSCNQEDHVSMGGFAARKALTVVEHVEAVLAMELLAACQGIEFLKPLISTAPLHKIYQLVRS-VAP nrõlaqpavvdnevtsalõedhlslgtsaalklgralenirrilaieyllaaqafeeflapqregogtäaawgilrervpa nkolshpasvdstptsanõedhvsmachgarrllqmtenlesiigiealaavāgiefraplttspelqkaaāavrgvsss nkalshphsvdslptsanõedhvsmapaagkriwēmaēntrgvlaiewigacõgldirkgiktsaklekaroalrsevah NKALAHPASVDSLPTSANÕEDHVSMAPNAGKRLWAMAENVRGILAVEWLGACÕGLDFREGLKSSPKLEQARŘLLRDKVPY NYTLAHPASVDSIPSSANQEDHVSMGTIGSRHAYQIIQNVRNVLAIELICAMQAVDIRGREKMASFTKKILEKGREHVPY nkīlahpasvdsipssanõedhvsmgtiaarhayqviantrviaieaicalõaveyrgiehaasytkolfqemrkvvps NKTLAHPASVDSLPTSANQEDHVSMATFAARRLRDMGENTRGILAVEYLAAAQGLDFRAPLKSSPRIEEARQILREKVPF nkõmshpasvdstptsanõedhvsmachgarrllamtdnlfgilgiealaavõgvelrgplktspelekaaavlrsavbv NKQMSHPASVDSTPTSANOEDHVSMACHGARRLLAMTDNLFGILGIEALAAVOGVELRGPLKTSPELEKAAAVLRSAVPV NKVLSHPASVDSIPTSANQEDHVSMGAHAARQLRQIVANVQTVLSIELLCAAQGLDFQQ-LRAGRGVQAAYEYVRTFVPT LKRLAVPASADSIPSSAMÕEDHVSMGWSAARKLRTAVDNLARVIAVELYAATRAIQLREGLTPAPASQAVVEAVRAAVEG MKRLAVPASADSIPSSAMÕEDHVSMGWSAARKLRTAVDNLARIVAVELYAATRAIĒLRAALTPAPASĒAVVAALRAAGAĞ NKRLAVPASVDSIPSSAMQEDHVSLGWHAARKLRTSVANLRRILAVEMLIAGRALDLRAPLKPGPATGAVLEVLRSKVAG

> 39.8% 38.9% 42.2% 38.68 38.6% 38.2% 38.8% 41.0% 40.78 39.2% 41.78 41.78 39.3% 40.48 42.28 46.8% 65.48 42.0% 66.18 13 SWALL: HUTH\_CAEEL . 14 SWALL: HUTH\_CAEEL . 15 SWALL: Q9HLI6 16 SWALL: HUTH MOUSE 17 SWALL: BAB29407 10 SWALL: HUTH PSEPU 11 SWALL: HUTH RHIME 18 SWALL:HUTH RAT 19 SWALL:AAG53586 SWALL:HUTH\_BACSU SWALL:Q9KSQ4 SWALL:HUTH\_STRGR SWALL:HUTH\_DEIRA SWALL: Q9KKEO SWALL:09HQD5 4 SWALL:BAB16159  $SWALL:Q9HU\overline{9}0$ SWALL:CAC21618 SWALL: Q9KBE6 SWALL:09HU85 SWALL: Q9KWE4 983831 9 œ

## Figure 14, cont'd.

		481	[ . 5 . ] 513
	983831	100.08	PGQDRFLSAELEAAYDLLANGSVHKALEAHLPA
	SWALL:CAC21618	66.18	PGPDRHLAPDLAAADAFVRAGHLVAAAESVTGP
.,	2 SWALL: HUTH STRGR	65.48	PGPDRFLAPDLAAADTFVREGRLVAAVEPVTGP
(,,	SWALL: HUTH_DEIRA	46.8%	LTEDRYFRPDLLRLRGELVSGRVAQAADTQAPA
7	4 SWALL:BAB16159	42.0%	LEDDRYMATDLKAAIEVVASGALVSAISSGLPV
υ,	5 SWALL:Q9KWE4	42.0%	LEDDRYMATDLKAAIEVVASGALVSAISSGLPV
w	6 SWALL: HUTH BACSU	40.48	IQQDRVFSYDIERLTDWLKKESLIPDHQNKELR
1~	7 SWALL: Q9KSQ4	42.28	YDKDRYFAPDIEKANALL-QLAVHNRLMPDQLL
ω	8 SWALL:Q9HU85	41.78	YQEDRFFAPDIEAASQLLASGCLNALLPARLLP
O1	9 SWALL:Q9KBE6	39.3%	IDQDRMFAKDIERAAKWLKDGSWDFTKMREKER
10	SWALL: HUTH PSEPU	41.78	YDRDRFFAPDIEKAVELLAKGSLTGLLPAGLPS
11	SWALL: HUTH RHIME	40.68	IEEDRYMADDLKAAGDLVASGRLAAAVSAGLPK
12	SWALL:Q9HU90	40.78	YDTDRWLAPDIASAAAILGERKSLARLAASIGD
13	SWALL: HUTH HUMAN	39.28	WIKDRFMAPDIEAAHRLLLEQKVWEVAAPYIEK
1.4	SWALL: HUTH CAEEL	38.8%	PNEDRYMKPEIDAVLEMIRENRIWEAVLPHLET
1.5	SWALL:Q9HLI6	41.0%	LDHDRPPSFDIETIRKMMDKKEFISALP
1.6	SWALL: HUTH MOUSE	38.68	WIKDRFMAPDIEAAHRLLLDQKVWEVAAPYIEK
1.7	SWALL:BAB29407	38.6%	WIKDRFMAPDIEAAHRLLLDQKVWEVAAPYIEK
18	SWALL: HUTH RAT	38.2%	WIKDRFMAPDIEAAHRLLLDQKVWEVAAPYIEK
19	SWALL: AAG53586	39.8%	YDDDRFFAPDIEAAISLLNKGSLVGLLPAFL
20	SWALL:Q9KKE0	38.9%	PIATIVR
2.1	. SWALL:Q9HQD5	42.28	PAGDRALADDMAAVGDLVRAGLVEDAVARALDA

## Figure 14, cont'd.

HAL

983831

,-	CAC21618	•	Strentomines colling
4	01017040	•	straptonily on controller
7	HUTH_STRGR	••	Streptomyces griseus
m	HUTH DEIRA	••	Deinococcus radiodurans
4	BAB16159	••	Agrobacterium rhizogenes
Ŋ	Q9KWE4	••	Agrobacterium rhizogenes
9	HUTH BACSU	• •	Bacillus subtilis
7	Q9KS <u>Q</u> 4	• •	Vibrio cholerae
ω	Q9HU85	• •	Pseudomonas aeruginosa
თ	Q9KBE6	••	Bacillus halodurans
10	HUTH PSEPU	• •	Pseudomonas putida
11	HUTH_RHIME	••	Rhizobium meliloti
12	06UH6Q	••	Pseudomonas aeruginosa
13	HUTH HUMAN	• •	Human
14	HUTH CAEEL	• •	Caenorhabditis elegans
15	$09HL\overline{1}6$	••	Thermoplasma acidophilum
16	HUTH MOUSE	• •	Mouse
17	BAB29407	• •	Mus musculus (Mouse)
18	HUTH_RAT	••	Rat
18	AAG53586	• •	uncultured bacterium pCosAS1
20	Q9KKE0	• •	Rhizobium meliloti
21	09H0D5	• •	Halobacterium sp

### igure 15

DOMESTAL GATEOT

STRG "HAL"	9	VVVGTSGTTAEDVVAVARHGARVELSAAAVEALAAARLIVDALAAKPEPVYGVSTGFGAL ITLGLSGATADDVIAVARHEARISISPQVLEELASVRAHIDALASADTPVYGISTGFGAL * ** ** ** ** ***********************
STRG, HAL	99	ASRHIGTELRAQLQRNIVRSHAAGMGPRVEREVVRALMFLRLKTVASGHTGVRPEVAQTM ATRHIAPEDRAKLQRSLIRSHAAGMGEPVEREVVRALMFLRAKTLASGRTGVRPVVLETM * ***
STRG HAL	126	ADVLNAGITPVVHEYGSLGCSGDLAPLSHCALTLMGEGEAEGPDGTVRPAGELLAAHGIA VGMLNAGITPVVREYGSLGCSGDLAPLSHCALVLMGEGEATDAHGDIRPVPELFAEAGLT ******* *****************************
STRG HAL	186 187	PVELREKEGLALLNGTDGMLGMLVMALADLRNLYTSADITAALSLEALLGTDKVLAPELH PVELAEKEGLALVNGTDGMLGQLIMALADLDELLDIADATAAMSVEAQLGTDQVFRAELH **** *********** * ****** * **********
STRG HAL	246 247	A-IRPHPGQGVSADNMSRVLAGSGLTGHHQDDAPRVQDAYSVRCAPQVNGAGRDTLDHAA EPLRPHPGQGRSAQNMFAFLADSPIVASHREGDGRVQDAYSLRCSPQVTGAARDTIAHAR ****** ** ** ** ** ** ** ** **********
STRG HAL	305	LVAGRELASSVDNPVVLPDGRVESNGNFHGAPVAYVLDFLAIVAADLGSICERRTDRLLD LVATRELAAAIDNPVVLPSGEVTSNGNFHGAPVAYVLDFLAIAVADLGSIAERRTDRMLD *** **** **** ****** * * ************

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DRFLAPDLAAADTFVREGRLVAAVE DRFLSAELEAAYDLLANGSVHKALE

485 484

STRG HAL

## Figure 15, Cont'd.

STRG	365	KNRSHGLPPFLADDAGVDSGLMIAQYTQAALVSEMKRLAVPASADSIPSSAMQEDHVSMG
HAL	367	PARSRDLPAFLADDPGVDSGMMIAQYTQAGLVAENKRLAVPASVDSIPSSAMQEDHVSLG
		* ********* *** ***** * ** ** ***** * *** *** ** ** **
STRG	425	WSAARKLRTAVDNLARIVAVELYAATRAIELRAAEGLTPAPASEAVVAALRAAGAEGPGP
HAL	427	WHAARKLRTSVANLRRILAVEMLIAGRALDLRAPLKPGPATGAVLEVLRSKVA-GPGQ